

10/019823  
USPTO Rec'd PCT/PTO 21 DEC 2001

SYN-128.ST25

SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic Combinations Thereof

<130> SYN-128

<140> PCT/GB00/02457

<141> 2000-06-23

<150> GB 9915215.9

<151> 1999-06-29

<150> GB 9930536.9

<151> 1999-12-23

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<170> FastSEQ for Windows Version 4.0

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Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys

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Arg

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Arg

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ccggacttcg ctgcatacgcc ggcgtcaacg taagtccacca tggatctggc aagcggagacc 180  
ataaacatgac gcagtatact aaccctggcc gttatagaac aagggtgtga gtcgacatgt 240  
tktacaacctt ctacaaacgc ggcactaat gacaacggtt gtgcggtaa ttcttagtgc 300  
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ccggacttcg ctgcatacgcc ggcgtcaacg taagtccacca tcctgacacgc acgtgaaggc 180  
aatgtactga ccctggccgt tatagaacaa gggttgtgat cgacatgtt tacaacctct 240  
acaaaacgcgc gcactaatga caacggtagt gccgtaatt ctatgtcgc aacttttgag 300  
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ccggacttcg ctgcacatcgcc ggcgtcaacg taagtaccca tcctgacacg acgtgaaggc 180  
aatgtactga ccctggccgt tatagaacaa gtttgtagt cgacatgttt tacaacctct 240  
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gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcggcgc cgcctcccg 120  
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gagatccagg ccggcaagat ctgcactct gctggagtt tttgtttctg cttctacctt 120  
tgatatatataataatata tcattaatata gtagtaataat aatatttcaa atatttttt 180  
caaaaataaaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgtatatt 240  
ttaatttctaa actttctaa tatatgacca aaacatggtg atgttttagaa atgtcccgcg 300  
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taa 363

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tgatataatat ataataatta tcattaatta gtatgtatataat aatatttcaa atatttttt 180  
caaaataaaaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgtatatt 240  
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccgcg 300  
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taa 363

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gagatccagg cccgcaagat ctgcaccccg gccggcgtgg ttgtttctg cttctacctt 120  
tgatataatat ataataatta tcattaatta gtatgtatataat aatatttcaa atatttttt 180  
caaaataaaaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgtatatt 240  
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa gtgccccggcc 300  
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tga 363

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ctccctgctgg agttgtacgt attttcatcc attttctyca ccactccctt aacatgaagc 180  
aactttctct tctctctaga aatgtcccgcc ggctcttccct tgctgccccgg gacttcgctg 240  
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gtataactaac cctggccgtt atagaacaag gttgtgagtc gacatgtkt acaacctcta 360  
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<400> 22  
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<400> 23  
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<210> 24  
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<400> 24

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 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr  
 370 375 380  
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg  
 385 390 395 400  
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn  
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 Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile Ala  
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 Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln Leu  
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 450 455 460  
 Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser Ala  
 465 470 475 480  
 Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala Asp  
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 Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu Val  
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 Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro Gly  
 515 520 525  
 Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly  
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 Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg Val  
 545 550 555 560  
 Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser Ile  
 565 570 575  
 Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn Arg  
 580 585 590  
 Gly Glu Asp Leu Asp Tyr Lys Thr Phe Xaa Thr Val Gly Phe Thr Thr  
 595 600 605  
 Pro Phe Ser Leu Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala Trp  
 610 615 620  
 Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val  
 625 630 635 640  
 Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala Gln  
 645 650 655  
 Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu Lys  
 660 665 670  
 Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu  
 675 680 685  
 Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe Glu  
 690 695 700  
 Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met  
 705 710 715

<210> 55  
 <211> 719  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; PROTEIN cry1Ia2 Embl. Accession No. M98544

&lt;400&gt; 55

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala  
 1 5 10 15  
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile  
 20 25 30  
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr  
 35 40 45  
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile  
 50 55 60  
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly  
 65 70 75 80  
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys  
 85 90 95  
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile  
 100 105 110  
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu  
 115 120 125  
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser  
 130 135 140  
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser  
 145 150 155 160  
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe  
 165 170 175  
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala  
 180 185 190  
 Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys  
 195 200 205  
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln  
 210 215 220  
 Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser  
 225 230 235 240  
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg  
 245 250 255  
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val  
 260 265 270  
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr  
 275 280 285  
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His  
 290 295 300  
 Pro His Pro Ser Phe Thr Ser Thr Trp Tyr Asn Asn Ala Pro  
 305 310 315 320  
 Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu  
 325 330 335  
 Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser  
 340 345 350  
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg  
 355 360 365  
 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr  
 370 375 380  
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg  
 385 390 395 400  
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn  
 405 410 415  
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile

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420                    425                    430  
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln  
435                    440                    445